

SPLICE FORM 1:

```

1  CGTCCTTCCT GGTCCCTGCGG GTCCAGGACT GTCCGCGGGG TTGAGGGAAG
51  GGGCCGTGCC CGGTGCCAGC CCAGGTGCTC GCGGCCTGGC TCCATGGCCC
101 TGGTCACAGT GAGCCGTTCG CCCCCGGGCA GCGGCGCCTC CACGCCCGTG
151 GGGCCCTGGG ACCAGGCGGT CCAGCGAAGG AGTCGACTCC AGCGAAGGCA
201 GAGCTTTGCG GTGCTCCGTG GGGCTGTCTT GGGACTGCAG GATGGAGGGG
251 ACAATGATGA TGCAGCAGAG GCCAGTCTTG AGCCAACAGA GAAGGCCCCG
301 AGTGAGGAGG AGCTCCACGG GGACCAGACA GACTTCGGGC AAGGATCCCA
351 GAGTCCCCAG AAGCAGGAGG AGCAGAGGCA GCACCTGCAC CTCATGGTAC
401 AGTCGGGTG GCGCAGGAT GACATCCGCC TGGCAGCCCA GCTGGAGGCA
451 CCCCCGCCCT CCGGCTCCG CTACCTGCTG GTAGTTTCTA CACGAGAAGG
501 AGAAGGTCTG AGCCAGGATG AGACGGTCCT CCTGGGCGTG GATTTCCTTG
551 ACAGCAGCTC CCCCAGCTGC ACCCTGGGCC TGGTCTTGCC CCTCTGGAGT
601 GACACCCAGG TGTACTTAGA TGGAGACGGG GGCTTCAGCG TGACGTCTGG
651 TGGGCAAAAG CGGATCTTCA AGCCCATCTC CATCCAGACC ATGTGGGCCA
701 CACTCCAGGT ATTGCACCAA GCATGTGAGG CAGCTCTAGG CAGCGGCCTT
751 GTACCGGGTG GCAGTGCCCT CACCTGGGCC AGCCACTACC AGGAGAGACT
801 GAACTCCGAA CAGAGCTGCC TCAATGAGTG GACGGCTATG GCCGACCTGG
851 AGTCTCTGCG GCCTCCACG GCGGAGCCTG GCGGGTCCTC AGAACAGGAG
901 CAGATGGAGC AGGCGATCCG TGCTGAGCTG TGGAAAGTGT TGGATGTCAG
951 TGACCTGGAG AGTGTCACCT CCAAAGAGAT CCGCCAGGCT CTGGAGCTGC
1001 GCCTGGGGCT CCCCCTCCAG CAGTACCGTG ACTTCATCGA CAACCAGATG
1051 CTGCTGCTGG TGGCAGACGG GGACCGAGCC TCCGCGCATC TCCCCACCT
1101 CTACCTGGGC TCAGAGTGGA ACGCAGCAAA CCTGGAGGAG CTGCAGAGGA
1151 ACAGGGTCAC CCACATCTTG AACATGGCCC GGGAGATTGA CAACTTCTAC
1201 CCTGAGCGCT TCACCTACCA CAATGTGCGC CTCTGGGATG AGGAGTCGGC
1251 CCAGCTGCTG CCGCACTGGA AGGAGACGCA CCGCTTCATT GAGGCTGCAA
1301 GAGCACAGGG CACCCACGTG CTGGTCCACT GCAAGATGGG CGTCAGCCGC
1351 TCAGCGGCCA CAGTGCTGGC CTATGCCATG AAGCAGTACG AATGCAGCCT
1401 GGAGCAGGCC CTGCGCCACG TGCAGGAGCT CCGGCCCATC GCCCGCCCCA
1451 ACCCTGGCTT CCTGCGCCAG CTGCAGATCT ACCAGGGCAT CCTGACGGCC
1501 AGAACCTGAG GGTGGTGGGG AGGAGAAGGT TGTAGGCATG GAAGAGAGCC
1551 AGGCAGCCCC GAAAGAAGAG CCTGGGCCAC GGCCACGTAT AAACCTCCGA
1601 GGGGTCATGA GGTCCATCAG TCTTCTGGAG CCCTCCTTGG AGCTGGAGAG
1651 CACCTCAGAG ACCAGTGACA TGCCAGAGGT CTCTCTTCC CACGAGTCTT
1701 CACATGAAGA GCCTCTGACA CCCTTCCCAC AGCTTGCAAG GACCAAGGGA
1751 GGCCAGCAGG TGGACAGGGG GCCTCAGCCT GCCCTGAAGT CCCGCCAGTC
1801 AGTGGTTACC CTCCAGGGCA GTGCCGTGGT GGCCAACCGG ACCCAGGCCT
1851 TCCAGGAGCA GGAGCAGGGG CAGGGGCAGG GGCAGGGAGA GCCCTGCATT
1901 TCCTCTACGC CCAGGTTCOG GAAGGTGGTG AGACAGGCCA GCGTGCATGA
1951 CAGTGGAGAG GAGGGCGAGG CCTGAGCCCT CACACATGCC CACGCTCCCC
2001 TGACACTGAA GAGGATCCAC AACTCCTTGG AGAAACACCC TCACGTCTGT
2051 TGCCGACAC ATTCCTCTCA GCTCCGCCCC ATACCCGTCA CTACAGCCTC
2101 ACCTCCCACC CCTGTCACTA CGGCCTCACC TCCCACCCTT GTCACTACAG
2151 CCTCACCTCC TACAGCCTTA AGTCCCAGGC CCATGTCTGC CTGTCCAAGG
2201 GCTCAAGACT TTCTAACTGG GATGTGGTAG AGGGACTGAA GGTACCTTTG
2251 GGGGCAACAG CACCCTAGTT TCATTCTCAA CTCTAGCCCT GCACACTCAC
2301 CTGTGGCAGC GAATGAAAAC AGAGCTTCCC GTGCAAAAAG GGTACGCCTT
2351 CCCACCCCGG CCCCTCCCT GCACCTCCTG TCCTCTCCA GTTCATTCTT
2401 GGAACCCAGC AGGCCAGGCA ACCAGTGGCC CCCAAAGGCA GGCAGGATCC
2451 TCAGGCCCCA GCCGCGGGAG GCTGGAAGGG CTGGCAGATC GCTTCCCTCA
2501 TCCACCTCCA CCGGTCCAGG TCTTTGCTGC TGTCCCAGA CCTCCTGTGA
2551 CACCACGCCA GATCACAGGG CACCAGGCCA GAGATAGTCT TCTTTTGTG
2601 CTTTCTGGCC TCTGGCTAGT CAGTTTTTCA TAGCCTTACA GTATCTGGCT
2651 TTGTACTGAG AAATAAAACA CATTTTCATA AAAAAAAAAA AAAAAAAAAA
2701 AAAA

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FEATURES:

5' UTR: 1-93
 Start: 94-1506
 Stop: 1509
 3' UTR: 1510-2704

SPLICE FORM 2:

1 TGGTTGAGGG AAGGGGCCGT GCCCGGTGCC AGCCAGGTG CTCGCGGCCT
51 GGCTCCATGG CCCTGGTCAC AGTGAGCCGT TCGCCCCCGG GCAGCGGCGC
101 CTCCACGCCC GTGGGGCCCT GGGACCAGGC GGTCCAGCGA AGGAGTCGAC
151 TCCAGCGAAG GCAGAGCTTT GCGGTGCTCC GTGGGGCTGT CCTGGGACTG
201 CAGGATGGAG GGGACAATGA TGATGCAGCA GAGGCCAGTT CTGAGCCAAC
251 AGAGAAGGCC CCGAGTGAGG AGGAGCTCCA CGGGGACCAG ACAGACTTCG
301 GGCAAGGATC CCAGAGTCCC CAGAAGCAGG AGGAGCAGAG GCAGCACCTG
351 CACCTCATGG TACAGCTGCT GAGGCCGAG GATGACATCC GCCTGGCAGC
401 CCAGCTGGAG GCACCCCGGC CTCCCCGGCT CCGCTACCTG CTGGTAGTTT
451 CTACACGAGA AGGAGAAGGT CTGAGCCAGG ATGAGACGGT CCTCCTGGGC
501 GTGGATTTCC CTGACAGCAG CTCCCCAGC TGCACCCTGG GCCTGGTCTT
551 GCCCTCTGG AGTGACACCC AGGTGTACTT AGATGGAGAC GGGGGCTTCA
601 GCGTGACGTC TGGTGGGCAA AGCCGGATCT TCAAGCCCAT CTCCATCCAG
651 ACCATGTGGG CCACACTCCA GGTATTGCAC CAAGCATGTG AGGCAGCTCT
701 AGGCAGCGGC CTTGTACCGG GTGGCAGTGC CCTCACCTGG GCCAGCCACT
751 ACCAGGAGAG ACTGAACTCC GAACAGAGCT GCCTCAATGA GTGGACGGCT
801 ATGGCCGACC TGGAGTCTCT GCGGCCCTCC AGCGCCGAGC CTGGCGGGTC
851 CTCAGAACAG GAGCAGATGG AGCAGGCGAT CCGTGCTGAG CTGTGGAAAG
901 TGTTGGATGT CAGTGACCTG GAGAGTGTCA CTTCCAAAGA GATCCGCCAG
951 GCTCTGGAGC TGCGCCTGGG GCTCCCCCTC CAGCAGTACC GTGACTTCAT
1001 CGACAACCCAG ATGCTGCTGC TGGTGGCACA GCGGGACCGA GCCTCCGCA
1051 TCTTCCCCCA CCTCTACTTG GGCTCAGAGT GGAACGCAGC AAACCTGGAG
1101 GAGCTGCAGA GGAACAGGGT CACCCACATC TTGAACATGG CCCGGGAGAT
1151 TGACAACTTC TACCCTGAGC GCTTACCTA CCACAATGTG CGCCTCTGGG
1201 ATGAGGAGTC GGCCAGCTG CTGCCGCACT GGAAGGAGAC GCACCGCTTC
1251 ATTGAGGCTG CAAGAGCACA GGGCACCCAC GTGCTGGTCC ACTGCAAGAT
1301 GGGCGTCAGC CGCTCAGCGG CCACAGTGCT GGCCTATGCC ATGAAGCAGT
1351 ACGAATGCAG CCTGGAGCAG GCCCTGCGCC ACGTGCAGGA GCTCCGGCCC
1401 ATCGCCCCGCC CCAACCCTGG CTTCTGCGC CAGCTGCAGA TCTACCAGGG
1451 CATCCTGACG GCCAGCCGCC AGAGCCATGT CTGGGAGCAG AAAGTGGGTG
1501 GGGTCTCCCC AGAGGAGCAC CCAGCCCCTG AAGTCTCTAC ACCATTCCCA
1551 CTTCTTCCGC CAGAACCTGA GGTGGTGGG GAGGAGAAGG TTGTAGGCAT
1601 GGAAGAGAGC CAGGCAGCCC CGAAAGAAGA GCCTGGGCCA CGGCCACGTA
1651 TAAACCTCCG AGGGGTCTATG AGGTCCATCA GTCTTCTGGA GCCCTCCTTG
1701 GAGCTGGAGA GCACCTCAGA GACCAGTGAC ATGCCAGAGG TCTTCTCTTC
1751 CCACGAGTCT TCACATGAAG AGCCTCTGCA GCCCTTCCCA CAGCTTGCAA
1801 GGACCAAGGG AGGCCAGCAG GTGGACAGGG GGCCTCAGCC TGCCCTGAAG
1851 TCCCGCCAGT CAGTGGTTAC CCTCCAGGGC AGTGCCCTGG TGCCAACCG
1901 GACCCAGGCC TTCCAGGAGC AGGAGCAGGG GCAGGGGCAG GGGCAGGGAG
1951 AGCCCTGCAT TTCTCTACG CCCAGGTTCC GGAAGGTGGT GAGACAGGCC
2001 AGCGTGCAATG ACAGTGGAGA GGAGGGCGAG GCCTGAGCCC TCACACATGC
2051 CCACGCTCCC CTGACACTGA AGAGGATCCA CAACTCCTTG GAGAAACACC
2101 CTCACGTCTG TTGCCGCACA CATTCCTCTC AGCTCCGCCC CATAACCGTC
2151 ACTACAGCCT CACCTCCAC CCTGTCACT ACGGCTCAC CTCCCACCCC
2201 TGCTACTACA GCCTCACCTC TTTCTAACTG GGATGTGGTA GAGGGACTGA
2251 CCTGTCCAAG GGCTCAAGAC TTTCTAACTG TTCATTCTCA ACTCTAGCCC
2301 AGGTACCTTT GGGGGCAACA GCACCCTAGT TTCATTCTCA ACTCTAGCCC
2351 TGCACACTCA CCTGTGGCAC GGAATGAAAA CAGAGCTTCC CGTGCAAAAA
2401 GGGTCACGCC TCCCACCCCC GCCCCCTCCC TGCACCTCCT GTCCTCTCCC
2451 AGTTCATTC TGGAAACCAGC CAGGCCAGGC AACCAGTGGC CCCCAAAGGC
2501 AGGCAGGATC CTCAGGCCCC AGCCGCGGGA GGCTGGAAGG GCTGGCAGAT
2551 CGCTTCCCTC ATCCACCTCC ACCGGTCCAG GTCTTTGTG CTGTCCCCAG
2601 ACCTCCTGTG ACACCACGCC AGATCACAGG GCACCAGGCC AGAGATAGTC
2651 TTCTTTTTGT CCTTCTGGC CTCTGGCTAG TCAGTTTTTC ATAGCCTTAC
2701 AGTATCTGGC TTTGTACTGA GAAATAAAAC ACATTTTCAT AAAAAAAAAA
2751 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2801 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2851 AA

FIGURE 1, page 2 of 5

FEATURES:

5' UTR: 1-56

Start: 57

Stop: 2034

3' UTR: 2037-2852

SPLICE FORM 3:

1 CCTGGTCTCTG CGGGTCCAGG ACTGTCCCGC GGGGTTGAGG GAAGGGGCCG
51 TGCCCGGTGC CAGCCCAGGT GCTCGCGGCC TGGTCCATG GCCCTGGTCA
101 CAGTGAGCCG TTCGCCCCG GGCAGCGGCG CCTCCACGCC CGTGGGGCCC
151 TGGGACCAGG CGGTCCAGCG AAGGAGTCGA CTCCAGCGAA GGCAGAGCTT
201 TGCGGTGCTC CGTGGGGCTG TCCTGGGACT GCAGGATGGA GGGGACAATG
251 ATGATGCAGC AGAGGCCAGT TCTGAGCCAA CAGAGAAGGC CCCGAGTGAG
301 GAGGAGCTCC ACGGGGACCA GACAGACTTC GGGCAAGGAT CCCAGAGTCC
351 CCAGAAGCAG GAGGAGCAGA GGCAGCACCT GCACCTCATG GTACAGCTGC
401 TCTAGTCCGA GGATGACATC CGCCTGGCAG CCCAGCTGGA GGCACCCCGG
451 CCTCCCCGGC TCCGCTACCT GCTGGTAGTT TCTACACGAG AAGGAGAAGG
501 TCTGAGCCAG GATGAGACGG TCCTCCTGGG CGTGGATTTC CCTGACAGCA
551 GCTCCCCCAG CTGCACCTTG GGCCTGGTCT TGGCCCTCTG GAGTGACACC
601 CAGGTGTACT TAGATGGAGA CGGGGGCTTC AGCGTGACGT CTGGTGGGCA
651 AAGCCGGATC TTCAAGCCCA TCTCCATCCA GACCATGTGG TCCTCAGAAC
701 AGGAGCAGAT GGAGCAGGCG ATCCGTGCTG AGCTGTGGAA AGTGTGGAT
751 GTCAGTGACC TGGAGAGTGT CACTTCCAAA GAGATCCGCC AGGCTCTGGA
801 GCTGCGCCTG GGGCTCCCCC TCCAGCAGTA CCGTGACTTC ATCGACAACC
851 AGATGCTGCT GCTGGTGGCA CAGCGGGACC GAGCCTCCCG CATCTTCCCC
901 CACCTCTACC TGGGCTCAGA GTGGAACGCA GCAAACCTGG AGGAGCTGCA
951 GAGGAACAGG GTCACCCACA TCTTGAACAT GGCCCGGGAG ATTGACAAC
1001 TCTACCCTGA GCGCTTCACC TACCACAATG TGCGCCTCTG GGATGAGGAG
1051 TCGGCCAGG GTCTGCCAGT CTGGAAGGAG ACGCACCGCT TCATTGAGGC
1101 TGCAAGAGCA CAGGGCACCC ACGTGCTGGT CCACTGCAAG ATGGGCGTCA
1151 GCCGCTCAGC GGCCACAGTG CTGGCCTATG CCATGAAGCA GTACGAATGC
1201 AGCCTGGAGC AGGCCCTGCG CCACGTGCAG GAGCTCCGGC CCATCGCCCG
1251 CCCCACCCCT GGCTTCCTGC GCCAGCTGCA GATCTACCAG GGCATCCTGA
1301 CGGCCAGAAC CTGAGGGTGG TGGGGAGGAG AAGGTTGTAG GCATGGAAGA
1351 GAGCCAGGCA GCCCCGAAAG AAGAGCCTGG GGCCACGGGG CACGTATAAA
1401 CCTCCGAGGG GTCATGAGGT CCATCAGTCT TCTGGAGCCC TCCTTGGGAG
1451 CTGGAGAGCA CCTCAGTAGA CCAGTGACAT GCCAGAGGTC TTCTCTTCCC
1501 ACGAGTCTTC ACATGAAGAG CCTCTGCAGC CCTTCCACA GCTTGCAAGG
1551 ACCAAGGGAG GCCAGCAGGT GGACAGGGGG CCTCAGCCTG CCCTGAAGTC
1601 CCGCCAGTCA GTGGTTACCC TCCAGGGCAG TGCCGTGGTG GCCAACCAGG
1651 CCCAGGCCTT CCAGGAGCAG GAGCAGGGGC AGGGGCAGGG GCAGGGAGAG
1701 CCTTGCATTT CCTCTACGCC CAGGTTCGGG AAGGTGGTGA GACAGGCCAG
1751 CGTGCATGAC AGTGAGAGAG AGGGCGAGGC CTGAGCCCTC ACACATGCCC
1801 ACGCTCCCCT GACACTGAAG AGGATCCACA ACTCCTTGGA GAAACACCCT
1851 CACGTCTGTT GCCGCACACA TTCCTCTCAG CTCCGCCCCA TACCCGTCAC
1901 TACAGCCTCA CCTCCCACCC CTGTCACTAC GGCCCTACCT CCCACCCCTG
1951 TCACTACAGC CTCACCTCCT ACAGCCTTAA GTCCCAGGCC CATGTCTGCC
2001 TGTTCAAGGG CTCAAGACTT TCTAACTGGG ATGTGGTAGA GGGACTGAAG
2051 GTACCTTTGG GGGCAACAGC ACCCTAGTTT CATTCTCAAC TCTAGCCCTG
2101 CACACTCACC TGTGGCACGG AATGAAAACA GAGCTTCCCG TGCAAAAAGG
2151 GTCACGCCTC CCACCCCGC CCCCTCCCTG CACCTCCTGT CCTCTCCAG
2201 TTCATTCTCT GAACCAGCCA GGCCAGGCAA CCAGTGGCCC CCAAAGGCAG
2251 GCAGGATCCT CAGGCCCCAG CCGCGGGAGG CTGGAAGGGC TGGCAGATCG
2301 CTTCCTCAT CCACCTCCAC CGGTCCAGGT CTTTGCTGCT GTCCCCAGAC
2351 CTTCTGTGAC ACCACGCCAG ATCACAGGGC ACCAGGCCAG AGATAGTCTT
2401 CTTTTTGTCC TTTCTGGCCT CTGGCTAGTC AGTTTTTCAT AGCCTTACAG
2451 TATCTGGCTT TGTACTGAGA AATAAAACAC ATTTTCATAT TTGGTTAAAA
2501 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

FEATURES:

5' UTR: 1-88
Start: 88
Stop: 1311
3' UTR: 1315-2540

Homologous proteins:**Top 10 BLAST Hits**

	Score	E
SPLICE FORM 1:		
gi 8923483 ref NP_060327.1 hypothetical protein FLJ20515 >gi 7...	576	e-163
gi 6714641 dbj BAA89534.1 (AB036834) MAP kinase phosphatase [D...	337	2e-91
gi 8922777 ref NP_060746.1 hypothetical protein FLJ10928 >gi 7...	233	3e-60
gi 7242951 dbj BAA92536.1 (AB037719) KIAA1298 protein [Homo sa...	143	4e-33
gi 7301242 gb AAF56372.1 (AE003750) CG6238 gene product [Droso...	124	2e-27
gi 4150963 emb CAA77232.1 (Y18620) DsPTP1 protein [Arabidopsis...	113	5e-24
gi 9294518 dbj BAB02780.1 (AB023036) dual-specificity protein ...	113	5e-24
gi 6862915 gb AAF30304.1 AC018907_4 (AC018907) putative dual-sp...	94	2e-18
gi 6015037 sp O54838 DUS5_RAT DUAL SPECIFICITY PROTEIN PHOSPHAT...	92	9e-18
gi 9910432 ref NP_064570.1 mitogen-activated protein kinase ph...	90	3e-17

SPLICE FORM 2:

gi 8923483 ref NP_060327.1 hypothetical protein FLJ20515 [Homo...	576	e-163
gi 6714641 dbj BAA89534.1 (AB036834) MAP kinase phosphatase [D...	340	6e-92
gi 8922777 ref NP_060746.1 hypothetical protein FLJ10928 [Homo...	229	1e-58
gi 7242951 dbj BAA92536.1 (AB037719) KIAA1298 protein [Homo sa...	162	1e-38
gi 9294518 dbj BAB02780.1 (AB023036) dual-specificity protein ...	113	8e-24
gi 4150963 emb CAA77232.1 (Y18620) DsPTP1 protein [Arabidopsis...	113	8e-24
gi 4758212 ref NP_004411.1 dual specificity phosphatase 8 [Hom...	99	3e-19
gi 6679156 ref NP_032774.1 neuronal tyrosine/threonine phospho...	96	2e-18
gi 6862915 gb AAF30304.1 AC018907_4 (AC018907) putative dual-sp...	94	6e-18
gi 6015037 sp O54838 DUS5_RAT DUAL SPECIFICITY PROTEIN PHOSPHAT...	92	2e-17

SPLICE FORM 3:

gi 8923483 ref NP_060327.1 hypothetical protein FLJ20515 [Homo...	410	e-113
gi 8922777 ref NP_060746.1 hypothetical protein FLJ10928 [Homo...	233	7e-60
gi 6714641 dbj BAA89534.1 (AB036834) MAP kinase phosphatase [D...	224	5e-57
gi 7242951 dbj BAA92536.1 (AB037719) KIAA1298 protein [Homo sa...	143	5e-33
gi 9294518 dbj BAB02780.1 (AB023036) dual-specificity protein ...	113	1e-23
gi 4150963 emb CAA77232.1 (Y18620) DsPTP1 protein [Arabidopsis...	113	1e-23
gi 6862915 gb AAF30304.1 AC018907_4 (AC018907) putative dual-sp...	94	5e-18
gi 6015037 sp O54838 DUS5_RAT DUAL SPECIFICITY PROTEIN PHOSPHAT...	92	2e-17
gi 9910432 ref NP_064570.1 mitogen-activated protein kinase ph...	90	7e-17
gi 9911130 gb AAA64693.2 (U15932) protein phosphatase [Homo sa...	90	1e-16

BLAST to dbEST:**SPLICE FORM 1:**

	Score	E
gi 9807071 /dataset=dbest /taxon=960...	1404	0.0
gi 10317998 /dataset=dbest /taxon=96...	1316	0.0
gi 10151079 /dataset=dbest /taxon=96...	1249	0.0
gi 10401153 /dataset=dbest /taxon=960...	1180	0.0
gi 10329921 /dataset=dbest /taxon=96...	1124	0.0
gi 7632969 /dataset=dbest /taxon=960...	791	0.0
gi 9155111 /dataset=dbest /taxon=9606...	779	0.0
gi 10994242 /dataset=dbest /taxon=96...	450	e-124

EXPRESSION INFORMATION FOR MODULATORY USE:

SPLICE FORM 1:

library source:

Expression information from BLAST dbEST hits:

gi 9807071	Human Pancreas
gi 10317998	Human colon adenocarcinoma
gi 10151079	Human Pancreas:adenocarcinoma
gi 10401153	Human Pancreas:epithelioid carcinoma
gi 10329921	Human lung: large cell carcinoma
gi 7632969	Human kidney: renal cell carcinoma
gi 9155111	Human Placenta choriocarcinoma
gi 10994242	Human ovary tumor tissue

Expression information from PCR-based tissue screening panels:

Human Brain
Human Fetal brain
Human fetal heart
Human fetal kidney
Human heart
Human kidney
Human uterus
Human thyroid

SPLICE FORM 1:

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1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFV LRGAVLGLQD
51 GGDNDAAEA SSEPTEKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
101 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDETVLLGVD
151 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
201 WATLQVLHQA CEALGSGLV PGGSALTWAS HYQERLNSEQ SCLNEWTAMA
251 DLESLRPPSA EPGGSSEQEQ MEQAIRAEW KVLVDSDLES VTSKEIRQAL
301 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
351 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
401 AARAQGTHVL VHCKMGVSR S AATVLAYAMK QECSLEQAL RHVQELRPIA
451 RPNPGFLRQL QIYQGILTAR T

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(SEQUENCE NO. 4)

SPLICE FORM 2:

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1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFV LRGAVLGLQD
51 GGDNDAAEA SSEPTEKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
101 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDETVLLGVD
151 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
201 WATLQVLHQA CEALGSGLV PGGSALTWAS HYQERLNSEQ SCLNEWTAMA
251 DLESLRPPSA EPGGSSEQEQ MEQAIRAEW KVLVDSDLES VTSKEIRQAL
301 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
351 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
401 AARAQGTHVL VHCKMGVSR S AATVLAYAMK QECSLEQAL RHVQELRPIA
451 RPNPGFLRQL QIYQGILTAS RQSHVWEQKV GGVSPPEEHPA PEVSTPFPLL
501 PPEPEGGGEE KVVGMEESSA APKEEPPGRP RINLRGVMRS ISLLEPSLEL
551 ESTSETSDMP EVFSSHESSH EEPLQPFQQL ARTKGGQQVD RGPQPALKSR
601 QSVVTLQGSA VVANRTQAFQ EQEQQGQGGQ GEPCISSTPR FRKVVRQASV
651 HDSGEGEEA

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(SEQUENCE NO. 5)

SPLICE FORM 3:

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1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFV LRGAVLGLQD
51 GGDNDAAEA SSEPTEKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
101 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDETVLLGVD
151 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
201 WSSEQEQQEQ AIRAELWKVL DVSDLESVTS KEIRQAELRL LGLPLQQYRD
251 FIDNQMLLLV AQRDRASRIF PHLYLGSEWN AANLEELQRN RVTHILNMAR
301 EIDNFYPERF TYHNVRLWDE ESAQLLPHWK ETHRFIEAAR AQGTHVLVHC
351 KMGVSRSAAT VLAYAMKQYE CSLEQALRHV QELRPIARN PGFLRQLQIY
401 QGILTART

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(SEQUENCE NO. 6)

FEATURES:

Functional domains and key regions:

SPLICE FORM 1:

[1] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

34-37 RRQS

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 6

1	65-67	TEK
2	132-134	STR
3	254-256	SLR
4	292-294	TSK
5	395-397	THR
6	468-470	TAR

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 6

1	70-73	SEEE
2	132-135	STRE
3	140-143	SQDE
4	266-269	SEQE
5	286-289	SDLE
6	292-295	TSKE

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

363-369 REIDNFY

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 8

1	12-17	GSGAST
2	43-48	GAVLGL
3	47-52	GLQDGG
4	218-223	GLVPGG
5	223-228	GSALTW
6	339-344	GSEWNA
7	416-421	GVSRSA
8	465-470	GILTAR

BLAST Alignment to Top Hit:

SPLICE FORM 1:

>gi|8923483|ref|NP_060327.1| hypothetical protein FLJ20515
 >gi|7020674|dbj|BAA91228.1| (AK000522) unnamed protein
 product [Homo sapiens]
 Length = 394

Score = 576 bits (1469), Expect = e-163
 Identities = 290/312 (92%), Positives = 296/312 (93%), Gaps = 1/312 (0%)

Query: 1 MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEA 60
 MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEA
 Sbjct: 1 MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEA 60

Query: 61 SSEPTEKAPSEEEELHGDQTDGFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAP 120
 SSEPTEKAPSEEEELHGDQTDGFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAP
 Sbjct: 61 SSEPTEKAPSEEEELHGDQTDGFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAP 120

Query: 121 RPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDSSSPSCTLGLVLPWSDTQVYLDGDGG 180
 RPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDSSSPSCTLGLVLPWSDTQVYLDGDGG
 Sbjct: 121 RPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDSSSPSCTLGLVLPWSDTQVYLDGDGG 180

Query: 181 FSVTSGGQSRIKFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASHYQERLNSEQ 240
 FSVTSGGQSRIKFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASHYQERLNSEQ
 Sbjct: 181 FSVTSGGQSRIKFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASHYQERLNSEQ 240

Query: 241 SCLNEWTAMADLESIRPPSAEPGGSSEQEQQEQAIRAELWKVLDV-SDLESVTSKEIRQA 299
 SCLNEWTAMADLESIRPPSAEPGGSSEQEQQEQAIRAELWKVL++ S E+ E+ +
 Sbjct: 241 SCLNEWTAMADLESIRPPSAEPGGSSEQEQQEQAIRAELWKVLELESTSETSDMPEVFSS 300

Query: 300 LELRLGLPLQQY 311
 E PLQ +
 Sbjct: 301 HESSHEEPLQPF 312

>gi|6714641|dbj|BAA89534.1| (AB036834) MAP kinase phosphatase
 [Drosophila melanogaster]
 Length = 1045

Score = 337 bits (854), Expect = 2e-91
 Identities = 204/537 (37%), Positives = 284/537 (51%), Gaps = 81/537 (15%)

Query: 1 MALVTVSRSPPGSGA-STPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAE 59
 MALVTV RSP +G+ S G + R + F +G L L
 Sbjct: 1 MALVTVQRSPSVAGSCSNSDGESEDDGNSKGNDRSECFAGKGTALVL----- 49

Query: 60 ASSEPTEKAPSEEEELHGDQTDGFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEA 119
 A + SE L D T +QS + + HL M LL+ +D +++A +LE+
 Sbjct: 50 ALKDIPPLTQSERRLSTDSTRSSNSTQS--NNSDIQLHLQSMFYLLQREDTLKMAVKLES 107

Query: 120 PRPPRLRYLLV-----VSTREGEGLSQDETVLLGVDFPDSSSPS----- 158
 R R RYL++ S R + + +V +G SS S
 Sbjct: 108 QRSNRTRYLVIA SRSCCRSGTSDRRRHRIMRHHSVKVGG SAGTKSSTSPAVPTQRQLSVE 167

Query: 159 -----CTLGL-----VLPLWSDTQVY 174
 C LG+ V+P+ +DT ++
 Sbjct: 168 QTATEASSKCDKTADKENATAAGDNKNTSGMEESCLLGIDCNERTTIGLVVPILADTTIH 227

Query: 175 LDGDGGFSVTSGGQSRIKFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASHYQE 234
 LDGDGGFSV ++ IFKP+S+Q MW+ LQ LH+ + A + G + W S Y+
 Sbjct: 228 LDGDGGFSVKVYEKTHIFKPVSVQAMWSALQTLHKVSKKAREN NFYASGPSHDWLSSYER 287

Query: 235 RLNSEQSCLEWTAMADLES LRPPSAEP--GGSSSEQMEQAIRAELWKVLDVSDLESVT 292
 R+ S+QSCLEW AM LES RPPS + E+E+ E I+ +L ++ DL+ VT
 Sbjct: 288 RIESDQSCLEWNAWDALESRRPPSPDAIRNKPPKEETESVIKMKLKAIMMSVDLDEV 347

Query: 293 SKEIRQALELRLGLPLQQYRDFIDNQMLLLVAQRDRASRIFPHLYLGSEWNAANLEELQR 352
 SK IR LE L + L +Y+ FID +ML+++ Q D ++IF H+YLGSEWNA+NLEELQ+
 Sbjct: 348 SKYIRGRLEEILDMDLGEYKSFIDAEMLVILGQMDAPTKIFEHVLYLGSEWNASNLEELQK 407

Query: 353 NRVTHILNMAREIDNFYPERFTYHNVRWLDEESAQLLPHWKETHRFIEAARAQGTHVLVH 412
 N V HILN+ REIDNF+P F Y NVR++D+E LL +W +T R+I A+A+G+ VLVH
 Sbjct: 408 NGVRHILNVTREIDNFFPGTFEYFNVRVYDDEKTNLLKYWDDTFRYITRAKAEGSKVLVH 467

Query: 413 CKMGVSRSAATVLAYAMKQYECSEALRHVQELRPIARPNGFLRQLQIYQGILTA 469
 CKMGVSRSA+ V+AYAMK Y+ +QAL HV++ R +PN FL QL+ Y G+L A
 Sbjct: 468 CKMGVSRASVVIAYAMKAYQWFEQQALEHVKKRRSCKIPNKNFLNQLLETYSGLDA 524

>gi|8922777|ref|NP_060746.1| hypothetical protein FLJ10928
 >gi|7023283|dbj|BAA91913.1| (AK001790) unnamed protein
 product [Homo sapiens]
 Length = 141

Score = 233 bits (588), Expect = 3e-60
 Identities = 111/111 (100%), Positives = 111/111 (100%)

Query: 361 MAREIDNFYPERFTYHNVRWLDEESAQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRS 420
 MAREIDNFYPERFTYHNVRWLDEESAQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRS
 Sbjct: 31 MAREIDNFYPERFTYHNVRWLDEESAQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRS 90

Query: 421 AATVLAYAMKQYECSEALRHVQELRPIARPNGFLRQLQIYQGILTART 471
 AATVLAYAMKQYECSEALRHVQELRPIARPNGFLRQLQIYQGILTART
 Sbjct: 91 AATVLAYAMKQYECSEALRHVQELRPIARPNGFLRQLQIYQGILTART 141

CHROMOSOME MAP POSITION:
Bac accession number: AP001885
Chromosome #: 11

ALLELIC VARIANTS (SNPs):

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
577	G	A	Exon	162	G	S
1451	G	A	Exon	453	S	N
2641	G	A	Beyond ORF (3')			

Context:

DNA

Position

577 TCTGAGCCAACAGAGAAGGCCCGAGTGAGGAGGAGCTCCACGGGGACCAGACAGACTTC
GGGCAAGGATCCCAGAGTCCCAGAAGCAGGAGGAGCAGAGGCAGCACCTGCACCTCATG
GTACAGCTGCTGAGGCCGCGAGGATGACATCCGCCTGGCAGCCCAGCTGGAGGCACCCCGG
CCTCCCCGGCTCCGCTACCTGCTGGTAGTTTCTACACGAGAAGGAGAAGGTCTGAGCCAG
GATGAGACGGTCTCCTGGGCGTGGAATTTCCCTGACAGCAGCTCCCCAGCTGCACCTGT
[G,A]
GCCTGGTCTTGCCCTCTGGAGTGACACCCAGGTGTACTTAGATGGAGACGGGGGCTTCA
GCGTGACGTCTGGTGGGCAAAGCCGGATCTTCAAGCCCATCTCCATCCAGACCATGTGGG
CCACACTCCAGGTATTGCACCAAGCATGTGAGGCAGCTCTAGGCAGCGGCCTTGTACCGG
GTGGCAGTGCCCTCACCTGGGCCAGCCACTACCAGGAGAGACTGAACTCCGAACAGAGCT
GCCTCAATGAGTGACGCGCTATGGCCGACCTGGAGTCTCTGCGGCCTCCAGCGCCGAGC

1451 ACAGGGTCACCCACATCTTGAACATGGCCCCGGGAGATTGACAACTTCTACCCTGAGCGCT
TCACCTACCACAATGTGCGCCTCTGGGATGAGGAGTCGGCCCCAGCTGCTGCCGCACTGGA
AGGAGACGCACCGCTTCATTGAGGCTGCAAGAGCACAGGGCACCCACGTGCTGTTCCACT
GCAAGATGGGCGTCAGCCGCTCAGCGGCCACAGTGCTGGCCTATGCCATGAAGCAGTACG
AATGCAGCCTGGAGCAGGCCCTGCGCCACGTGCAGGAGCTCCGGCCCATCGCCCGCCCCA
[G,A]
CCCTGGCTTCCTGCGCCAGCTGCAGATCTACCAGGGCATCCTGACGGCCAGAACCTGAGG
GTGGTGGGGAGGAGAAGGTTGTAGGCATGGAAGAGAGCCAGGCAGCCCCGAAAGAAGAGC
CTGGGCCACGGCCACGTATAAACCTCCGAGGGGTATGAGGTCCATCAGTCTTCTGGAGC
CCTCCTTGAGCTGGAGAGCACCTCAGAGACCAGTGACATGCCAGAGGTCTTCTCTTCCC
ACGAGTCTTCACATGAAGAGCCTCTGCAGCCCTTCCCACAGCTTGCAAGGACCAAGGGAG

2641 GGTCACGCCTCCACCCCCGCCCCCTCCCTGCACCTCCTGTCTCTCCAGTTCATTCT
GGAACCAAGCCAGGCCAGGCAACCAAGTGGCCCCCAAAGGCAGGCAGGATCCTCAGGCCCA
GCCGCGGGAGGCTGGAAGGGCTGGCAGATCGCTTCCCTCATCCACCTCCACCGTCCAGG
TCTTTGCTGCTGTCCCCAGACCTCCTGTGACACCACGCCAGATCACAGGGCACCAGGCCA
GAGATAGTCTTCTTTTGTCTTTCTGGCCTCTGGCTAGTCAGTTTTTCATAGCCTTACA
[G,A]
TATCTGGCTTTGTACTGAGAAATAAAACACATTTTCATAAAAAAAAAAAAAAAAAAAAAA
AAA

GENE STRUCTURE MODEL:

SPLICE FORM 2 5'-e1-e2-e3-e4-e5-e6-e7-e8-e9-e10-e11-e12-e13-e14-3'
SPLICE FORM 1 5'-e1-e2-e3-e4-e5-e6-e7-e8-e9-e10-e11-e12-----3'
SPLICE FORM 3 5'-e1-e2-e3-e4-e5-e6----e8-e9-e10-e11-e12-----3'

MULTIPLE ALIGNMENT OF CDNA SEQUENCES:

SPLICE FORM 2 ~~~~~~TG GTTGAGGGAA
SPLICE FORM 1 CGTCCTTCCT GGTCTGCGG GTCCAGGACT GT.CCGCGGG GTTGAGGGAA
SPLICE FORM 3 ~~~~~~CCT GGTCTGCGG GTCCAGGACT GTCCCGCGG GTTGAGGGAA

51 100
SPLICE FORM 2 GGGGCCGTGC CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC

		701				750
SPLICE	FORM 2	ACACTCCAGG	TATTGCACCA	AGCATGTGAG	GCAGCTCTAG	GCAGCGGCCT
SPLICE	FORM 1	ACACTCCAGG	TATTGCACCA	AGCATGTGAG	GCAGCTCTAG	GCAGCGGCCT
SPLICE	FORM 3
		751				800
SPLICE	FORM 2	TGTACCGGGT	GGCAGTGCCC	TCACCTGGGC	CAGCCACTAC	CAGGAGAGAC
SPLICE	FORM 1	TGTACCGGGT	GGCAGTGCCC	TCACCTGGGC	CAGCCACTAC	CAGGAGAGAC
SPLICE	FORM 3
		801				850
SPLICE	FORM 2	TGAACTCCGA	ACAGAGCTGC	CTCAATGAGT	GGACGGCTAT	GGCCGACCTG
SPLICE	FORM 1	TGAACTCCGA	ACAGAGCTGC	CTCAATGAGT	GGACGGCTAT	GGCCGACCTG
SPLICE	FORM 3
		851				900
SPLICE	FORM 2	GAGTCTCTGC	GGCCTCCCAG	CGCCGAGCCT	GGCGGGTCCT	CAGAACAGGA
SPLICE	FORM 1	GAGTCTCTGC	GGCCTCCCAG	CGCCGAGCCT	GGCGGGTCCT	CAGAACAGGA
SPLICE	FORM 3GGTCCT	CAGAACAGGA
		901				950
SPLICE	FORM 2	GCAGATGGAG	CAGGCGATCC	GTGCTGAGCT	GTGGAAAGTG	TTGGATGTCA
SPLICE	FORM 1	GCAGATGGAG	CAGGCGATCC	GTGCTGAGCT	GTGGAAAGTG	TTGGATGTCA
SPLICE	FORM 3	GCAGATGGAG	CAGGCGATCC	GTGCTGAGCT	GTGGAAAGTG	TTGGATGTCA
		951				1000
SPLICE	FORM 2	GTGACCTGGA	GAGTGTCACT	TCCAAAGAGA	TCCGCCAGGC	TCTGGAGCTG
SPLICE	FORM 1	GTGACCTGGA	GAGTGTCACT	TCCAAAGAGA	TCCGCCAGGC	TCTGGAGCTG
SPLICE	FORM 3	GTGACCTGGA	GAGTGTCACT	TCCAAAGAGA	TCCGCCAGGC	TCTGGAGCTG
		1001				1050
SPLICE	FORM 2	CGCCTGGGGC	TCCCCCTCCA	GCAGTACCGT	GACTTCATCG	ACAACCAGAT
SPLICE	FORM 1	CGCCTGGGGC	TCCCCCTCCA	GCAGTACCGT	GACTTCATCG	ACAACCAGAT
SPLICE	FORM 3	CGCCTGGGGC	TCCCCCTCCA	GCAGTACCGT	GACTTCATCG	ACAACCAGAT
		1051				1100
SPLICE	FORM 2	GCTGCTGCTG	GTGGCACAGC	GGGACCGAGC	CTCCCGCATC	TTCCCCCACC
SPLICE	FORM 1	GCTGCTGCTG	GTGGCACAGC	GGGACCGAGC	CTCCCGCATC	TTCCCCCACC
SPLICE	FORM 3	GCTGCTGCTG	GTGGCACAGC	GGGACCGAGC	CTCCCGCATC	TTCCCCCACC
		1101				1150
SPLICE	FORM 2	TCTACCTGGG	CTCAGAGTGG	AACGCAGCAA	ACCTGGAGGA	GCTGCAGAGG
SPLICE	FORM 1	TCTACCTGGG	CTCAGAGTGG	AACGCAGCAA	ACCTGGAGGA	GCTGCAGAGG
SPLICE	FORM 3	TCTACCTGGG	CTCAGAGTGG	AACGCAGCAA	ACCTGGAGGA	GCTGCAGAGG
		1151				1200
SPLICE	FORM 2	AACAGGGTCA	CCCACATCTT	GAACATGGCC	CGGGAGATTG	ACAACTTCTA
SPLICE	FORM 1	AACAGGGTCA	CCCACATCTT	GAACATGGCC	CGGGAGATTG	ACAACTTCTA
SPLICE	FORM 3	AACAGGGTCA	CCCACATCTT	GAACATGGCC	CGGGAGATTG	ACAACTTCTA
		1201				1250
SPLICE	FORM 2	CCCTGAGCGC	TTCACCTACC	ACAATGTGCG	CCTCTGGGAT	GAGGAGTCGG
SPLICE	FORM 1	CCCTGAGCGC	TTCACCTACC	ACAATGTGCG	CCTCTGGGAT	GAGGAGTCGG
SPLICE	FORM 3	CCCTGAGCGC	TTCACCTACC	ACAATGTGCG	CCTCTGGGAT	GAGGAGTCGG
		1251				1300
SPLICE	FORM 2	CCCAGCTGCT	GCCGCACTGG	AAGGAGACGC	ACCGCTTCAT	TGAGGCTGCA
SPLICE	FORM 1	CCCAGCTGCT	GCCGCACTGG	AAGGAGACGC	ACCGCTTCAT	TGAGGCTGCA
SPLICE	FORM 3	CCCAGCTGCT	GCCGCACTGG	AAGGAGACGC	ACCGCTTCAT	TGAGGCTGCA
		1301				1350
SPLICE	FORM 2	AGAGCACAGG	GCACCCACGT	GCTGGTCCAC	TGCAAGATGG	GCGTCAGCCG
SPLICE	FORM 1	AGAGCACAGG	GCACCCACGT	GCTGGTCCAC	TGCAAGATGG	GCGTCAGCCG

FIGURE 3, page 4 of 8

SPLICE FORM 3	AGAGCACAGG	GCACCCACGT	GCTGGTCCAC	TGCAAGATGG	GCGTCAGCCG
	1351				1400
SPLICE FORM 2	CTCAGCGGCC	ACAGTGCTGG	CCTATGCCAT	GAAGCAGTAC	GAATGCAGCC
SPLICE FORM 1	CTCAGCGGCC	ACAGTGCTGG	CCTATGCCAT	GAAGCAGTAC	GAATGCAGCC
SPLICE FORM 3	CTCAGCGGCC	ACAGTGCTGG	CCTATGCCAT	GAAGCAGTAC	GAATGCAGCC
	1401				1450
SPLICE FORM 2	TGGAGCAGGC	CCTGCGCCAC	GTGCAGGAGC	TCCGGCCCAT	CGCCCGCCCC
SPLICE FORM 1	TGGAGCAGGC	CCTGCGCCAC	GTGCAGGAGC	TCCGGCCCAT	CGCCCGCCCC
SPLICE FORM 3	TGGAGCAGGC	CCTGCGCCAC	GTGCAGGAGC	TCCGGCCCAT	CGCCCGCCCC
	1451				1500
SPLICE FORM 2	AACCCTGGCT	TCCTGCGCCA	GCTGCAGATC	TACCAGGGCA	TCCTGACGGC
SPLICE FORM 1	AACCCTGGCT	TCCTGCGCCA	GCTGCAGATC	TACCAGGGCA	TCCTGACG..
SPLICE FORM 3	AACCCTGGCT	TCCTGCGCCA	GCTGCAGATC	TACCAGGGCA	TCCTGACG..
	1501				1550
SPLICE FORM 2	CAGCCGCCAG	AGCCATGTCT	GGGAGCAGAA	AGTGGGTGGG	GTCTCCCCAG
SPLICE FORM 1
SPLICE FORM 3
	1551				1600
SPLICE FORM 2	AGGAGCACCC	AGCCCCTGAA	GTCTCTACAC	CATTCCCACT	TCTTCCGCCA
SPLICE FORM 1GCCA
SPLICE FORM 3GCCA
	1601				1650
SPLICE FORM 2	GAACCTGAGG	GTGGTGGGGA	GGAGAAGGTT	GTAGGCATGG	AAGAGAGCCA
SPLICE FORM 1	GAACCTGAGG	GTGGTGGGGA	GGAGAAGGTT	GTAGGCATGG	AAGAGAGCCA
SPLICE FORM 3	GAACCTGAGG	GTGGTGGGGA	GGAGAAGGTT	GTAGGCATGG	AAGAGAGCCA
	1651				1700
SPLICE FORM 2	GGCAGCCCCG	AAAGAAGAGC	CTGGG..CCA	CGGCCACGTA	TAAACCTCCG
SPLICE FORM 1	GGCAGCCCCG	AAAGAAGAGC	CTGGG..CCA	CGGCCACGTA	TAAACCTCCG
SPLICE FORM 3	GGCAGCCCCG	AAAGAAGAGC	CTGGGGCCAC	GGGGCACGTA	TAAACCTCCG
	1701				1750
SPLICE FORM 2	AGGGGTCATG	AGGTCCATCA	GTCTTCTGGA	GCCCTCCTT.	GGAGCTGGAG
SPLICE FORM 1	AGGGGTCATG	AGGTCCATCA	GTCTTCTGGA	GCCCTCCTT.	GGAGCTGGAG
SPLICE FORM 3	AGGGGTCATG	AGGTCCATCA	GTCTTCTGGA	GCCCTCCTTG	GGAGCTGGAG
	1751				1800
SPLICE FORM 2	AGCACCTCAG	.AGACCAGTG	ACATGCCAGA	GGTCTTCTCT	TCCCACGAGT
SPLICE FORM 1	AGCACCTCAG	.AGACCAGTG	ACATGCCAGA	GGTCTTCTCT	TCCCACGAGT
SPLICE FORM 3	AGCACCTCAG	TAGACCAGTG	ACATGCCAGA	GGTCTTCTCT	TCCCACGAGT
	1801				1850
SPLICE FORM 2	CTTCACATGA	AGAGCCTCTG	CAGCCCTTCC	CACAGCTTGC	AAGGACCAAG
SPLICE FORM 1	CTTCACATGA	AGAGCCTCTG	CAGCCCTTCC	CACAGCTTGC	AAGGACCAAG
SPLICE FORM 3	CTTCACATGA	AGAGCCTCTG	CAGCCCTTCC	CACAGCTTGC	AAGGACCAAG
	1851				1900
SPLICE FORM 2	GGAGGCCAGC	AGGTGGACAG	GGGGCCTCAG	CCTGCCCTGA	AGTCCCGCCA
SPLICE FORM 1	GGAGGCCAGC	AGGTGGACAG	GGGGCCTCAG	CCTGCCCTGA	AGTCCCGCCA
SPLICE FORM 3	GGAGGCCAGC	AGGTGGACAG	GGGGCCTCAG	CCTGCCCTGA	AGTCCCGCCA
	1901				1950
SPLICE FORM 2	GTCAGTGGTT	ACCCTCCAGG	GCAGTGCCGT	GGTGGCCAAC	CGGACCCAGG
SPLICE FORM 1	GTCAGTGGTT	ACCCTCCAGG	GCAGTGCCGT	GGTGGCCAAC	CGGACCCAGG
SPLICE FORM 3	GTCAGTGGTT	ACCCTCCAGG	GCAGTGCCGT	GGTGGCCAAC	CGGACCCAGG
	1951				2000

FIGURE 3, page 5 of 8

SPLICE FORM 2 CCTTCCAGGA GCAGGAGCAG GGGCAGGGGC AGGGGCAGGG AGAGCCCTGC
 SPLICE FORM 1 CCTTCCAGGA GCAGGAGCAG GGGCAGGGGC AGGGGCAGGG AGAGCCCTGC
 SPLICE FORM 3 CCTTCCAGGA GCAGGAGCAG GGGCAGGGGC AGGGGCAGGG AGAGCCCTGC

 2001 2050
 SPLICE FORM 2 ATTTCTCTA CGCCCAGGTT CCGGAAGGTG GTGAGACAGG CCAGCGTGCA
 SPLICE FORM 1 ATTTCTCTA CGCCCAGGTT CCGGAAGGTG GTGAGACAGG CCAGCGTGCA
 SPLICE FORM 3 ATTTCTCTA CGCCCAGGTT CCGGAAGGTG GTGAGACAGG CCAGCGTGCA

 2051 2100
 SPLICE FORM 2 TGACAGTGGA GAGGAGGGCG AGGCCTGAGC CCTCACACAT GCCCAGCTC
 SPLICE FORM 1 TGACAGTGGA GAGGAGGGCG AGGCCTGAGC CCTCACACAT GCCCAGCTC
 SPLICE FORM 3 TGACAGTGGA GAGGAGGGCG AGGCCTGAGC CCTCACACAT GCCCAGCTC

 2101 2150
 SPLICE FORM 2 CCCTGACACT GAAGAGGATC CACAACCTCCT TGGAGAAACA CCCTCACGTC
 SPLICE FORM 1 CCCTGACACT GAAGAGGATC CACAACCTCCT TGGAGAAACA CCCTCACGTC
 SPLICE FORM 3 CCCTGACACT GAAGAGGATC CACAACCTCCT TGGAGAAACA CCCTCACGTC

 2151 2200
 SPLICE FORM 2 TGTTGCCGCA CACATTCTC TCAGCTCCGC CCCATACCCG TCACTACAGC
 SPLICE FORM 1 TGTTGCCGCA CACATTCTC TCAGCTCCGC CCCATACCCG TCACTACAGC
 SPLICE FORM 3 TGTTGCCGCA CACATTCTC TCAGCTCCGC CCCATACCCG TCACTACAGC

 2201 2250
 SPLICE FORM 2 CTCACCTCCC ACCCCTGTCA CTACGGCCTC ACCTCCCACC CCTGTCACTA
 SPLICE FORM 1 CTCACCTCCC ACCCCTGTCA CTACGGCCTC ACCTCCCACC CCTGTCACTA
 SPLICE FORM 3 CTCACCTCCC ACCCCTGTCA CTACGGCCTC ACCTCCCACC CCTGTCACTA

 2251 2300
 SPLICE FORM 2 CAGCCTCACC TCCTACAGCC TTAAGTCCCA GGCCCATGTC TGCCTGTCCA
 SPLICE FORM 1 CAGCCTCACC TCCTACAGCC TTAAGTCCCA GGCCCATGTC TGCCTGTCCA
 SPLICE FORM 3 CAGCCTCACC TCCTACAGCC TTAAGTCCCA GGCCCATGTC TGCCTGTCCA

 2301 2350
 SPLICE FORM 2 AGGGCTCAAG ACTTTCTAAC TGGGATGTGG TAGAGGGACT GAAGGTACCT
 SPLICE FORM 1 AGGGCTCAAG ACTTTCTAAC TGGGATGTGG TAGAGGGACT GAAGGTACCT
 SPLICE FORM 3 AGGGCTCAAG ACTTTCTAAC TGGGATGTGG TAGAGGGACT GAAGGTACCT

 2351 2400
 SPLICE FORM 2 TTGGGGGCAA CAGCACCCTA GTTTCATTCT CAACTCTAGC CCTGCACACT
 SPLICE FORM 1 TTGGGGGCAA CAGCACCCTA GTTTCATTCT CAACTCTAGC CCTGCACACT
 SPLICE FORM 3 TTGGGGGCAA CAGCACCCTA GTTTCATTCT CAACTCTAGC CCTGCACACT

 2401 2450
 SPLICE FORM 2 CACCTGTGGC ACGGAATGAA AACAGAGCTT CCCGTGCAA AAGGGTCACG
 SPLICE FORM 1 CACCTGTGGC ACGGAATGAA AACAGAGCTT CCCGTGCAA AAGGGTCACG
 SPLICE FORM 3 CACCTGTGGC ACGGAATGAA AACAGAGCTT CCCGTGCAA AAGGGTCACG

 2451 2500
 SPLICE FORM 2 CCTCCCACCC CCGCCCCCTC CCTGCACCTC CTGTCCTCTC CCAGTTCATT
 SPLICE FORM 1 CCTCCCACCC CCGCCCCCTC CCTGCACCTC CTGTCCTCTC CCAGTTCATT
 SPLICE FORM 3 CCTCCCACCC CCGCCCCCTC CCTGCACCTC CTGTCCTCTC CCAGTTCATT

 2501 2550
 SPLICE FORM 2 CCTGGAACCA GCCAGGCCAG GCAACCAAGT GCCCCCAAAG GCAGGCAGGA
 SPLICE FORM 1 CCTGGAACCA GCCAGGCCAG GCAACCAAGT GCCCCCAAAG GCAGGCAGGA
 SPLICE FORM 3 CCTGGAACCA GCCAGGCCAG GCAACCAAGT GCCCCCAAAG GCAGGCAGGA

 2551 2600
 SPLICE FORM 2 TCCTCAGGCC CCAGCCGCGG GAGGCTGGAA GGGCTGGCAG ATCGCTTCCC
 SPLICE FORM 1 TCCTCAGGCC CCAGCCGCGG GAGGCTGGAA GGGCTGGCAG ATCGCTTCCC
 SPLICE FORM 3 TCCTCAGGCC CCAGCCGCGG GAGGCTGGAA GGGCTGGCAG ATCGCTTCCC

FIGURE 3, page 6 of 8

